

**Patent Claims**

1. Use of polypeptides with the biological activity of a very long chain fatty acid  
elongase for identifying herbicidally active compounds
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2. Use according to Claim 1, characterized in that the polypeptides are 60%  
homologous with the polypeptide according to SEQ ID NO: 2.
3. Use according to Claim 1, characterized in that the herbicidally active  
10 compounds are modulators of these polypeptides.
4. Use according to any one of Claims 1 to 3, characterized in that the  
polypeptides include a sequence which is selected from
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- a) the sequence shown in SEQ ID NO: 2,
- b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
- c) partial sequences of the sequences defined under a) or b) which still  
20 have the biological activity of a VLCFAE,
- d) sequences which have an identity of at least 60%, preferably of 80%,  
particularly preferably of 90%, with the sequences defined under a) to  
c),
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- e) sequences which include the C-terminally localized active site of the  
polypeptide shown in SEQ ID NO: 2,
- f) sequences which have an identity of at least 60%, preferably of 80%,  
30 particularly preferably of 90%, with the sequences defined under e),

g) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2,

h) sequences which have an identity of at least 60%, preferably of 80%, particularly preferably of 90%, with the sequences defined under g).

5. Use of nucleic acids which code for polypeptides with the biological activity of a very long chain fatty acid elongase in methods for identifying modulators of these polypeptides.

6. Use of nucleic acids which code for polypeptides with the biological activity of a very long chain fatty acid elongase for identifying substances which alter the expression of the polypeptides encoded by them.

7. Use according to Claim 5 or 6, characterized in that single-stranded or double-stranded DNA or RNA is involved.

8. Use according to Claim 5 or 6, characterized in that fragments of genomic DNA or cDNA are involved.

9. Use according to any of Claims 5 to 8, characterized in that the nucleic acids comprise a sequence which is selected from

a) the sequence shown in SEQ ID NO: 1,

b) sequences which code for a polypeptide including the amino acid sequence shown in SEQ ID NO: 2,

c) partial sequences at least 14 base-pairs long of the sequences defined under a) or b),

- d) sequences which hybridize to the sequences defined under a) or b),
- e) sequences which have an identity of at least 60%, preferably of 80%, particularly preferably of 90%, with the sequences defined under a) or b),
- f) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2
- g) sequences which have an identity of at least 60%, preferably of 80%, particularly preferably of 90%, with the sequences defined under f),
- h) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
- i) sequences which have an identity of at least 60%, preferably of 80%, particularly preferably of 90%, with the sequences defined under h),
- j) sequences which are complementary to the sequences defined under a) to i), and
- k) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to h).

10. Use of a DNA construct comprising a nucleic acid having SEQ ID NO: 1 and of a heterologous promoter in methods for identifying herbicidally active compounds.

11. Use of a vector comprising a nucleic acid having SEQ ID NO:1, in methods for identifying herbicidally active compounds.

12. Use of a host cell containing a nucleic acid coding for a polypeptide having  
SEQ ID NO: 2 in methods for identifying herbicidally active compounds.
- 5 13. Use according to Claim 12, characterized in that the host cell used is *E. coli*.
14. Use of a host cell according to claim 13, characterized in that a yeast, insect,  
mammalian or plant cell is involved.
- 10 15. Method for finding a chemical compound which binds to a polypeptide with  
the biological activity of a very long chain fatty acid elongase, comprising the  
following steps:
- 15 a) contacting a polypeptide with the biological activity of a very long  
chain fatty acid elongase or a host cell containing a polypeptide with a  
chemical compound or a mixture of chemical compounds under  
conditions which permit the interaction of a chemical compound with  
the polypeptide, and
- 20 b) determining the chemical compound which specifically binds to the  
polypeptide.
16. Method for finding inhibitors and/or activators of a polypeptide with the  
biological activity of a very long chain fatty acid elongase, comprising the  
25 following steps:
- 30 a) contacting a polypeptide with the biological activity of a very long  
chain fatty acid elongase or a host cell containing a polypeptide with a  
chemical compound or a mixture of chemical compounds under  
conditions which permit the interaction of a chemical compound with  
the polypeptide, and

- b) determining whether the activity of the polypeptide is reduced or increased by the chemical compound and, where appropriate,
- 5 c) determining the compound which specifically reduces or increases the activity of the polypeptide.
17. Method for finding a compound which alters the expression of polypeptides with the biological activity of a very long chain fatty acid elongase, comprising the following steps:
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- a) contacting a host cell containing a nucleic acid coding for a polypeptide with the biological activity of a very long chain fatty acid elongase with a chemical compound or a mixture of chemical compounds,
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- b) determining the polypeptide concentration and
- c) determining the compound which specifically influences the expression of the polypeptide.
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18. Use of the regulatory region which naturally controls the transcription of a nucleic acid having SEQ ID NO: 1 in plant cells, especially in Arabidopsis, in DNA constructs according to Claim 10, vectors according to Claim 11, host cells according to any of Claims 12 to 14 or in methods according to any of Claims 15 to 17.
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19. Use of a modulator of a polypeptide with the biological activity of a very long chain fatty acid elongase as plant growth regulator or herbicide.
- 30 20. Modulators of VLCFAE which are found by a method according to Claim 16 or 17.

21. Herbicidally active substances which are found by a method according to Claims 16 or 17.
- 5 22. Use of the nucleic acid coding for a polypeptide having SEQ ID NO: 2 for producing transgenic plants.
23. Transgenic plants, parts of plants, protoplasts, plant tissues or plant propagation materials, characterized in that, after introduction of a nucleic acid coding for a polypeptide having SEQ ID NO: 2, the intracellular concentration of a polypeptide according to Claim 14 is increased or reduced compared with the corresponding wild-type cells.
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24. Plants, parts of plants, protoplasts, plant tissues or plant propagation materials, characterized in that they contain a polypeptide having SEQ ID NO: 2 whose biological activity or expression pattern is altered by comparison with the corresponding endogenous polypeptides.
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